

Sheet 1 of 10

FORM PTO-1449 INFORMATION DISCLOSURE CITATION IN AN APPLICATION (Use several sheets if necessary)	Docket Number (Optional)	Application Number
	823.0093USQ	10/071,859
	Applicant	
	John R. Desjarlais	
Filing Date	Group Art Unit	
February 6, 2002	2857	

U. S. PATENT DOCUMENTS

EXAMINER INITIAL	DOCUMENT NUMBER	DATE	NAME	CLASS	SUBCLASS	FILING DATE IF APPROPRIATE
IJS/	5,965,408	10/12/99	Short	435	91.1	
	6,171,820	1/9/01	Short	435	69.1	
	5,939,250	8/17/99	Short	435	4	
	5,644,048	1/1/97	Yau	536	25.3	
	5,034,506	7/23/91	Summerton et al.	528	391	
	5,235,033	8/10/93	Summerton et al.	528	391	
	4,469,863	9/4/84	Ts'o et al.	536	27	
	5,216,141	6/1/93	Benner	536	27.13	
	5,602,240	2/11/97	De Mesmaeker et al.	536	22.1	
	5,637,684	6/10/97	Cook et al.	536	23.1	
	5,386,023	1/31/95	Sanghvi et al.	536	25.3	

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	DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUBCLASS	Translation	
						YES	NO
	WO 94/24314	10/27/94	PCT	C12Q	1/68		
	WO 97/27213	7/31/97	PCT	C07K	1/04		
	WO 97/27212	7/31/97	PCT	C07K	1/04		

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Sheet 2 of 10

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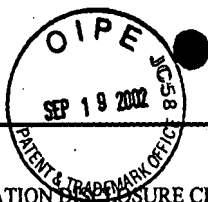
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					YES	NO

OTHER DOCUMENTS (including Author, Title, Date, Pertinent Pages, Etc.)

/JS/	Liwo et al. "A united-residue force field for off-lattice protein-structure simulations. I. Functional Forms and Parameters of long-range side-chain interaction potentials from protein crystal data." J. Comp. Chem., Vol. 18, No. 7, 849-873.
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/JS/	Fischer et al. "Protein fold recognition using sequence-derived predictions." Protein Science, Vol. 5, 1996, 947-955.
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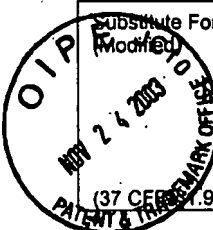
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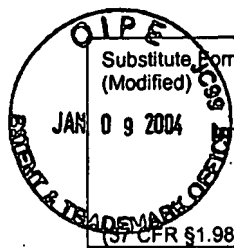
 Substitute Form PTO-1449 Modified Information Disclosure Statement by Applicant (Use several sheets if necessary) (37 CFR 1.98(b))	U.S. Department of Commerce Patent and Trademark Office		Attorney's Docket No. 16380-003001	Application No. 10/071,859
	Applicant John R. Desjarlais			
	Filing Date June 8, 2001		Group Art Unit 2857	

U.S. Patent Documents							
Examiner Initial	Design ID	Document Number	Publication Date	Patentee	Class	Subclass	Filing Date If Appropriate
/JS/	AA	US 6,188,965	Feb. 13, 2001	Mayo et al.			
/JS/	AB	US 6,269,312	Jul. 31, 2001	Mayo et al.			
/JS/	AC	US 6,403,312	Jun. 11, 2002	Dahiyat et al.			
/JS/	AD	US 2002/0123846	Sep. 5, 2002	Miller et al.			
	AE						
	AF						
	AG						
	AH						
	AI						
	AJ						
	AK						

Foreign Patent Documents or Published Foreign Patent Applications								
Examiner Initial	Design ID	Document Number	Publication Date	Country or Patent Office	Class	Subclass	Translation	
							Yes	No
	AL							
	AM							
	AN							
	AO							
	AP							

Other Documents (include Author, Title, Date, and Place of Publication)		
Examiner Initial	Design ID	Document
	AQ	
	AR	
	AS	
	AT	

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(Modified)U.S. Department of Commerce
Patent and Trademark OfficeAttorney's Docket No.
16380-003001Application No.
10/071,859**Information Disclosure Statement
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(Use several sheets if necessary)

(37 CFR §1.98(b))

Applicant
John R. DesjarlaisFiling Date
February 6, 2002Group Art Unit
1631**Other Documents (include Author, Title, Date, and Place of Publication)**

Examiner Initial	Desig. ID	Document
/JS/	AA	Dahiyat et al. "Automated design of the surface positions of protein helices." <i>Protein Science</i> . (1997), 6: 1333-1337.
	AB	Dahiyat et al. "Protein design automation." <i>Protein Science</i> . (1996), 5: 895-903.
	AC	Dahiyat et al. "De novo protein design: Fully automated sequence selection." <i>Science</i> . Vol. 278, 3 Oct. 1997, 82-87.
	AD	Dahiyat et al. "Probing the role of packing specificity in protein design." <i>Proc. Natl. Acad. Sci. USA</i> . Vol. 94, 10172-10177. Scot. 1997.
	AE	Dahiyat et al. "De novo protein design: Towards fully automated sequence selection." <i>J. Mol. Biol.</i> (1997)273, 789-796.
	AF	Delarue et al. "The inverse protein folding problem: Self consistent mean field optimisation of a structure specific mutation matrix." <i>Pac Symp Biocomput.</i> (1997), 109-121
	AG	Desjarlais et al. "Computer Search Algorithms in protein modification and design." (1998) <i>Curr Opin Struct Biol.</i> 8(4), 471-5.
	AH	Desjarlais et al. "De novo design of the hydrophobic cores of proteins." <i>Protein Science</i> (1995), 4,2006-18.
	AI	Desjarlais et al. "Side-chain and backbone flexibility in protein core design." <i>J. Mol. Biol.</i> (1999), 290(1), 305-18.
	AJ	Desmet et al., "The dead-end elimination theorem and its use in protein side-chain positioning." <i>Nature</i> . (1992), 356(9). 539-542.
	AK	Dunbrack et al. "Bayesian statistical analysis of protein side-chain rotamer preferences." <i>Protein Sci.</i> (1997) 6(8), 1661-81.
	AL	Eisenberg et al., "Solvation energy in protein folding and binding." <i>Nature</i> . 319(6050), 199-203.
	AM	Goldstein . "Efficient rotamer elimination applied to protein side-chains and related spin glasses." <i>Biophys. J.</i> (1994) 66(5), 1335-40.
	AN	Gordon. "Energy functions for protein design." <i>Curr Opin Struct Biol.</i> (1999), 9(4), 509-13.
	AO	Harbury et al. "Repacking protein cores with backbone freedom: structure prediction for coiled coils." <i>Proc Natl Acad Sci USA</i> . (1995), 92(18), 8408-12.
	AP	Hellinga. "Rational protein design: combining theory and experiment." <i>Proc Natl Acad Sci USA</i> . (1997), 94(19), 10015-17.

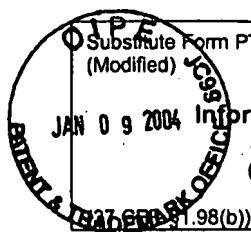
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 U.S. Department of Commerce
Patent and Trademark Office

 Attorney's Docket No.
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 Application No.
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**Information Disclosure Statement
by Applicant**

(Use several sheets if necessary)

 Applicant
John R. Desjarlais

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February 6, 2002

 Group Art Unit
1631

Other Documents (include Author, Title, Date, and Place of Publication)

Examiner Initial	Desig. ID	Document
IJS/	AQ	Hellinga et al. "Optimal sequence selection in proteins of known structure by simulated evolution." <i>Proc Natl Acad Sci USA</i> . (1994), 91(13), 5803-7.
	AR	Hendsch et al. "Electrostatic interactions in the GCN4 leucine zipper: Substantial contributions arise from intramolecular interactions enhanced on binding." <i>Protein Sci.</i> (1999)8(7), 1381-92.
	AS	Henikoff et al. "Position-based sequence weights." <i>J. Mol. Biol.</i> (1994) 243(4), 574-8.
	AT	Holland. "Adaptation in natural and artificial systems." <i>The MIT Press</i> , Cambridge, MA (1992).
	AU	Johnson et al. "Solution structure and dynamics of a designed hydrophobic core variant of ubiquitin." <i>Structure Fold Des.</i> (1999), 7(8), 967-76.
	AV	Jorgensen et al. "The OPLS potential functions for proteins. Energy minimizations for crystals of cyclic peptides and crambin." <i>J. Amer. Chem. Soc.</i> (1988), 110(6), 1657-1666.
	AW	Koehl et al. "Application of a self-consistent mean field theory to predict protein side-chains conformation and estimate their conformational entropy." <i>J. Mol. Biol.</i> , 239(2), 249-75.
	AX	Koehl et al. "Mean-field minimization methods for biological macromolecules." <i>Curr Opin Struct Biol.</i> , (1996), 6(2), 222-6.
	AY	Kono et al. "Energy minimization method using automata network for sequence and side-chain conformation prediction from given backbone geometry." <i>Proteins</i> . (1994), 19(3), 244-255.
	AZ	Kono et al. "Designing the hydrophobic core of <i>Thermus flavus</i> malate dehydrogenase based on side-chain packing." <i>Protein Eng.</i> (1998), 11(1), 47-52.
	AAA	Kuhlman et al. "Native protein sequences are close to optimal for their structures." <i>Proc. Natl. Acad. Sci. USA</i> . (2000), 97(19), 10383-8.
	ABB	Lazar et al. "De novo design of the hydrophobic core of ubiquitin." <i>Protein Sci.</i> (1997), 6(6), 1167-78.
	ACC	Lazar et al. "Rotamer strain as a determinant of protein structural specificity." <i>Protein Sci.</i> (1999), 8(12), 2598-610.
	ADD	Lee. "Predicting protein mutant energetics by self-consistent ensemble optimization." <i>J. Mol. Biol.</i> (1994), 236(3), 918-39.
	AEE	Micheletti et al. "Design of proteins with hydrophobic and polar amino acids." <i>Proteins</i> . (1998), 32(1), 80-7.
	AFF	Raha et al. "Prediction of amino acid sequence from structure." <i>Protein Sci.</i> (2000), 9(6), 1106-19.

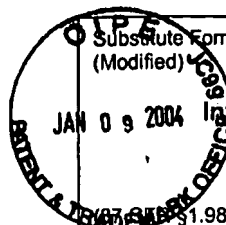
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Other Documents (include Author, Title, Date, and Place of Publication)

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/JSI/	AGG	Ranganathan et al. "Structural and functional analysis of the mitotic rotamase Pin1 suggests substrate recognition is phosphorylation dependent." <i>Cell</i> . (1997), 89(6), 875-86.
/JSI/	AHH	Street et al. "Computational protein design." <i>Structure Fold Des.</i> (1999), 7(5), R105-9.
/JSI/	AII	Su et al. "Coupling backbone flexibility and amino acid sequence selection in protein design." <i>Protein Sci.</i> (1997), 6(8), 1701-7.
/JSI/	AJJ	Voigt et al. "Trading accuracy for speed: A quantitative comparison of search algorithms in protein sequence design." <i>J. Mol. Biol.</i> (2000), 299(3), 789-803.
/JSI/	AKK	Voigt et al. "Computational method to reduce the search space for directed protein evolution." <i>Proc. Natl. Acad. Sci. USA.</i> (2001), 98(7), 3778-83.
/JSI/	ALL	Weiner et al. "A new force field for molecular mechanical simulation of nucleic acids and proteins." <i>Journal of the American Chemical Society.</i> (1984), 106(3), 765-84.

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